

## SEQUENCE LISTING

&lt;110&gt; Sode, Koji

&lt;120&gt; Glucose Dehydrogenase

&lt;130&gt; PSD-9014US

&lt;140&gt; PCT/JP2004/014575

&lt;141&gt; 2004-09-28

&lt;150&gt; JP 2003-340092

&lt;151&gt; 2003-09-30

&lt;160&gt; 6

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 1776

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; DNA coding for fugion protein

&lt;400&gt; 1

```

atgaataaac atttattggc taaaattgct ttattaagcg ctgttcagct agttacactc   60
tcagcatttg ctgatgttcc tctaactcca tctcaatttg ctaaagcgaa atcagagaac   120
tttgacaaga aagttattct atctaactta aataagccgc atgctttgtt atggggacca   180
gataatcaaa tttggttaac tgagcgagca acaggttaaga ttctaagagt taatccagag   240
tcgggtagtg taaaaacagt ttttcaggta ccagagattg tcaatgatgc tgatgggcag   300
aatggtttat taggttttgc cttccatcct gatttttaaaa ataatcctta tatctatatt   360
tcaggtagat ttaaaaatcc gaaatctaca gataaagaat taccgaacca aacgattatt   420
cgctgttata cctataataa atcaacagat acgctcgaga agccagtcga tttattagca   480
ggattacctt catcaaaaga ccatcagtcg ggtcgtcttg tcattgggcc agatcaaaaag   540
atattattata cgattggtga ccaagggcgt aaccagcttg cttatttggt cttgccaaat   600
caagcacaac atacgccaac tcaacaagaa ctgaatggta aagactatca cacctatatg   660
ggtaaagtac tacgcttaaa tcttgatgga agtattccaa aggataatcc aagttttaac   720
ggggtggtta gccatattta tacacttgga catcgtaatc cgcagggtt agcattcact   780
ccaaatggta aattattgca gtctgaacaa ggcccaaact ctgacgatga aattaacctc   840
attgtcaaag gtggcaatta tgggtggccg aatgtagcag gttataaaga tgatagtggc   900
tatgcttatg caaattattc agcagcagcc aataagtcaa ttaaggattt agctcaaaat   960
ggagtaaaaag tagccgcagg ggtccctgtg acgaaagaat ctgaatggac tggtaaaaac  1020
tttgtcccac cattaaaaac tttatatacc gttcaagata cctacaacta taacgatcca  1080
acttgtggag agatgaccta catttgctgg ccaacagttg caccgtcatc tgccatgtgc  1140

```

tataagggcg gtaaaaaagc aattactggt tgggaaaata cattattggt tccatcttta 1200  
 aaacgtggtg tcattttccg tattaagtta gatccaactt atagcactac ttatgatgac 1260  
 gctgtaccga tgtttaagag caacaaccgt tatcgtgatg tgattgcaag tccagatggg 1320  
 aatgtcttat atgtattaac tgatactgcc ggaaatgtcc aaaaagatga tggctcagta 1380  
 acaaatacat tagaaaaccc aggatctctc attaagttca cctataaggc taaggagctc 1440  
 ggcaaggcca ggatgccgga gttcgtggcc cagcgcaccg gccagttgct gcagggcgtg 1500  
 aaatacgacc ccgccaaggt cgaggccggc accatgctgt atgtggccaa ctgcgttttc 1560  
 tgtcacggcg tgcctggcgt ggaccgtggc ggaaacattc ccaatctggg ttacatggac 1620  
 gcgagctata tcgagaacct gccaaacttt gtcttcaagg gcccggccat ggtgcgcggc 1680  
 atgccggact tcacgggcaa gttgtcgggc gatgacgtgg agtccctcaa ggccttcac 1740  
 cagggcacgg cggacgccat ccggcccaag ccctga 1776

<210> 2

<211> 591

<212> PRT

<213> artificial sequence

<220>

<223> fugion protein

<400> 2

Met Asn Lys His Leu Leu Ala Lys Ile Ala Leu Leu Ser Ala Val Gln  
 1 5 10 15  
 Leu Val Thr Leu Ser Ala Phe Ala Asp Val Pro Leu Thr Pro Ser Gln  
 20 25 30  
 Phe Ala Lys Ala Lys Ser Glu Asn Phe Asp Lys Lys Val Ile Leu Ser  
 35 40 45  
 Asn Leu Asn Lys Pro His Ala Leu Leu Trp Gly Pro Asp Asn Gln Ile  
 50 55 60  
 Trp Leu Thr Glu Arg Ala Thr Gly Lys Ile Leu Arg Val Asn Pro Glu  
 65 70 75 80  
 Ser Gly Ser Val Lys Thr Val Phe Gln Val Pro Glu Ile Val Asn Asp  
 85 90 95  
 Ala Asp Gly Gln Asn Gly Leu Leu Gly Phe Ala Phe His Pro Asp Phe  
 100 105 110  
 Lys Asn Asn Pro Tyr Ile Tyr Ile Ser Gly Thr Phe Lys Asn Pro Lys  
 115 120 125  
 Ser Thr Asp Lys Glu Leu Pro Asn Gln Thr Ile Ile Arg Arg Tyr Thr  
 130 135 140

Tyr Asn Lys Ser Thr Asp Thr Leu Glu Lys Pro Val Asp Leu Leu Ala  
 145                      150                      155                      160  
 Gly Leu Pro Ser Ser Lys Asp His Gln Ser Gly Arg Leu Val Ile Gly  
                     165                      170                      175  
 Pro Asp Gln Lys Ile Tyr Tyr Thr Ile Gly Asp Gln Gly Arg Asn Gln  
                     180                      185                      190  
 Leu Ala Tyr Leu Phe Leu Pro Asn Gln Ala Gln His Thr Pro Thr Gln  
                     195                      200                      205  
 Gln Glu Leu Asn Gly Lys Asp Tyr His Thr Tyr Met Gly Lys Val Leu  
                     210                      215                      220  
 Arg Leu Asn Leu Asp Gly Ser Ile Pro Lys Asp Asn Pro Ser Phe Asn  
 225                      230                      235                      240  
 Gly Val Val Ser His Ile Tyr Thr Leu Gly His Arg Asn Pro Gln Gly  
                     245                      250                      255  
 Leu Ala Phe Thr Pro Asn Gly Lys Leu Leu Gln Ser Glu Gln Gly Pro  
                     260                      265                      270  
 Asn Ser Asp Asp Glu Ile Asn Leu Ile Val Lys Gly Gly Asn Tyr Gly  
                     275                      280                      285  
 Trp Pro Asn Val Ala Gly Tyr Lys Asp Asp Ser Gly Tyr Ala Tyr Ala  
                     290                      295                      300  
 Asn Tyr Ser Ala Ala Ala Asn Lys Ser Ile Lys Asp Leu Ala Gln Asn  
 305                      310                      315                      320  
 Gly Val Lys Val Ala Ala Gly Val Pro Val Thr Lys Glu Ser Glu Trp  
                     325                      330                      335  
 Thr Gly Lys Asn Phe Val Pro Pro Leu Lys Thr Leu Tyr Thr Val Gln  
                     340                      345                      350  
 Asp Thr Tyr Asn Tyr Asn Asp Pro Thr Cys Gly Glu Met Thr Tyr Ile  
                     355                      360                      365  
 Cys Trp Pro Thr Val Ala Pro Ser Ser Ala Tyr Val Tyr Lys Gly Gly  
                     370                      375                      380  
 Lys Lys Ala Ile Thr Gly Trp Glu Asn Thr Leu Leu Val Pro Ser Leu  
 385                      390                      395                      400  
 Lys Arg Gly Val Ile Phe Arg Ile Lys Leu Asp Pro Thr Tyr Ser Thr  
                     405                      410                      415  
 Thr Tyr Asp Asp Ala Val Pro Met Phe Lys Ser Asn Asn Arg Tyr Arg  
                     420                      425                      430

Asp Val Ile Ala Ser Pro Asp Gly Asn Val Leu Tyr Val Leu Thr Asp  
 435 440 445  
 Thr Ala Gly Asn Val Gln Lys Asp Asp Gly Ser Val Thr Asn Thr Leu  
 450 455 460  
 Glu Asn Pro Gly Ser Leu Ile Lys Phe Thr Tyr Lys Ala Lys Glu Leu  
 465 470 475 480  
 Gly Lys Ala Arg Met Pro Glu Phe Val Ala Gln Arg Thr Gly Gln Leu  
 485 490 495  
 Leu Gln Gly Val Lys Tyr Asp Pro Ala Lys Val Glu Ala Gly Thr Met  
 500 505 510  
 Leu Tyr Val Ala Asn Cys Val Phe Cys His Gly Val Pro Gly Val Asp  
 515 520 525  
 Arg Gly Gly Asn Ile Pro Asn Leu Gly Tyr Met Asp Ala Ser Tyr Ile  
 530 535 540  
 Glu Asn Leu Pro Asn Phe Val Phe Lys Gly Pro Ala Met Val Arg Gly  
 545 550 555 560  
 Met Pro Asp Phe Thr Gly Lys Leu Ser Gly Asp Asp Val Glu Ser Leu  
 565 570 575  
 Lys Ala Phe Ile Gln Gly Thr Ala Asp Ala Ile Arg Pro Lys Pro  
 580 585 590

<210> 3

<211> 38

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 3

ggccatggat aaacatttat tggctaaaat tgctttat

38

<210> 4

<211> 29

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 4

gggggagctc cttagcctta taggtgaac

29

<210> 5  
<211> 30  
<212> DNA  
<213> artificial sequence

<220>

<223> PCR primer

<400> 5

gggggagctc ggcaaggcca ggatgccgga

30

<210> 6

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> PCR primer

<400> 6

ggggaagctt tcagggttg ggccggatgg

30